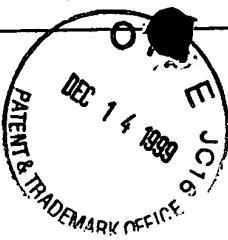


SEQUENCE LISTING



<110> Walker, Ameae M.

<120> PROLACTIN ANTAGONISTS AND USES THEREOF

<130> Walker_2500_097US2

<140> 09/065,330

<141> 1998-04-23

<150> PCT/US97/01435

<151> 1997-01-30

<150> 08/594,809

<151> 1996-01-31

<160> 6

<170> PatentIn Ver. 2.1

<210> 1

<211> 832

<212> DNA

<213> Homo sapiens

<220>

<221> mutation

<222> (622)..(624)

B1
<223> This is the codon for the substituted amino acids
of the mutated sequence.

<400> 1

aacatgaaca tcaaaggata gccatggaaa gggcccttc tgctgtgtc ggtgtcaaac 60
ctgctgtgt gccagagcgt ggcccccttg cccatctgtc cggcggggc tgcccgatgc 120
caggtagccc ttccgacacct gtttgcgc gccgtcgatc tgtccacta catccataac 180
ctctcctcag aaatgttcag cgaattcgat aaacggtata cccatggccg ggggttcatt 240
accaaggcca tcaacagctg ccacacttct tcccttgcca cccccaaga caaggagcaa 300
gccccaaacaga tgaatcaaaa agacttctg agcctgatag tcagcatatt gcgcattctgg 360
aatggaccc ttttatcatct ggtcacggaa gtacgtggta tgcaagaagc cccggaggct 420
atcctatcca aagctgtaga gattgaggag caaaccaac ggcttctaga gggcatggag 480
ctgatagtca gccaggttca tcctgaaacc aaagaaaaatg agatctaccc tttctgtcg 540
ggacttccat ccctgcagat ggctgtatgaa ggtctcgcc ttctgttta ttataacctg 600
ctccactgcc tacgcaggaa tnnncataaa atcgacaaatt atctcaagct cctgaagtgc 660
cgaatcatcc acaacaacaa ctgctaagcc cacatccatt tcatctattt ctgagaaggt 720
ccttaatgtat ccgttccatt gcaagcttct tttagttgtt tctctttga atccatgctt 780
gggtgtaaca ggtctcctct taaaaataa aaactgactc gtttagagaca tc 832

<210> 2
<211> 227
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (208)
<223> Site mutated codon where the normal codon coding
for serine is modified preferably to encode for
aspartate or glutamate, most preferably aspartate.

<400> 2
Asn Met Asn Ile Lys Gly Ser Pro Trp Lys Gly Ser Leu Leu Leu
1 5 10 15
Leu Val Ser Asn Leu Leu Cys Gln Ser Val Ala Pro Leu Pro Ile
20 25 30
Cys Pro Gly Gly Ala Ala Arg Cys Gln Val Thr Leu Arg Asp Leu Phe
35 40 45
Asp Arg Ala Val Val Leu Ser His Tyr Ile His Asn Leu Ser Ser Glu
50 55 60
Met Phe Ser Glu Phe Asp Lys Arg Tyr Thr His Gly Arg Gly Phe Ile
65 70 75 80
Thr Lys Ala Ile Asn Ser Cys His Thr Ser Ser Leu Ala Thr Pro Glu
85 90 95
Asp Lys Glu Gln Ala Gln Gln Met Asn Gln Lys Asp Phe Leu Ser Leu
100 105 110
Ile Val Ser Ile Leu Arg Ser Trp Asn Glu Pro Leu Tyr His Leu Val
115 120 125
Thr Glu Val Arg Gly Met Gln Glu Ala Pro Glu Ala Ile Leu Ser Lys
130 135 140
Ala Val Glu Ile Glu Glu Gln Thr Lys Arg Leu Leu Glu Gly Met Glu
145 150 155 160
Leu Ile Val Ser Gln Val His Pro Glu Thr Lys Glu Asn Glu Ile Tyr
165 170 175
Pro Val Trp Ser Gly Leu Pro Ser Leu Gln Met Ala Asp Glu Glu Ser

180

185

190

Arg Leu Ser Ala Tyr Tyr Asn Leu Leu His Cys Leu Arg Arg Asp Xaa
195 200 205

His Lys Ile Asp Asn Tyr Leu Lys Leu Leu Lys Cys Arg Ile Ile His
210 215 220

Asn Asn Asn Cys

225

<210> 3

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: This sequence
is a primer.

<400> 3

23

gcagggatga ccacaagg tt gac

D1
<210> 4

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: This sequence
is a primer.

<220>

<221> variation

<222> (12)

<223> This is a codon that can be replaced for nucleic
acid substitutes.

<400> 4

24

cgcaaggat gnacacaagg tt gac

<210> 5

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: This sequence
is a primer.

<220>

<221> variation

<222> (12)

<223> This is a codon that can be replaced for nucleic
acid substitutes.

<400> 5

acgcaggat gnkataaaat cg

22

B.
<210> 6

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: This sequence
is a primer.

<400> 6

cgtggccccc atatgttgcc catctg

26